

From: Romeo, David
Sent: Sunday, January 09, 2005 7:46 AM
To: STIC-Biotech/ChemLib
Subject: 10028051

Requester's Name: ... David Romeo
Serial Number: ... 10028051
Art Unit: ... 1647
Office: ... REM 4D39
Mailbox: ... REM 4C70
Phone: ... 571 272-0890
Date of Request: ... 01/09/05

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JAN 10 2005
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(STIC)

PLEASE PROVIDE RESULTS ON DISK(s)

Search the commercial/public and interference files for SEQ ID NO: 1.

Search the commercial/public and interference files for SEQ ID NO: 3.

Search the commercial/public and interference files for SEQ ID NO: 23.

STAFF USE ONLY

Searcher: ED HART

Searcher Phone: 2-

Date Searcher Picked up: 1/10/05

Date Completed: 1/11/05

Searcher Prep/Rev. Time: 11:00

Online Time:

Type of Search

NA Sequence: # 3

AA Sequence :#

Structure: #

Bibliographic:

Litigation:

Patent Family:

Other:

Vendors and cost where applicable

STN:

DIALOG:

QUESTEL/ORBIT:

LEXIS/NEXIS:

SEQUENCE SYSTEM: Qseq

WWW/Internet:

Other(Specify):

Run on: January 10, 2005, 11:50:10 ; Search time 9805.83 Seconds
 (without alignments)
 1148.874 Million cell updates/sec

Title: US-10-028-051A-1

Perfect score: 2374

Sequence: 1 aatagatggcgccggccag.....aaaaaaaaaaaaaaaaaa 2374

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ror:*

11: gb_sts:*

12: gb_sy:*

13: gb_uni:*

14: gb_vti:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2335	98.4	2351	4 BTU04164
2	1467.4	61.8	2039	6 AR129187 Sequence
3	1467.4	61.8	2039	6 AR447852 Sequence
4	1399.6	59.0	1920	6 BD192740 Secreted
5	1384.6	58.3	1909	6 AX339773 Sequence
6	1384.6	58.3	1909	9 HSU191903 Human
7	1376.4	58.0	1893	6 ARU16408 Sequence
8	1376.4	58.0	1893	6 BD195148 Endoderm,
9	1376.4	58.0	1893	9 HSU68057 Human
10	1123.8	47.3	1476	6 AX655712 Sequence
11	1122.8	47.3	1476	6 AX597112 Sequence
12	1122.8	47.3	1476	6 AX701367 Sequence
13	1122.8	47.3	1476	6 AX821908 Sequence
14	1122.8	47.3	1476	9 HSU44163 Human
15	1082.4	45.6	2814	10 BC016884
16	1070	45.1	2540	10 MMU088568 Mus
17	1055.2	44.4	1687	9 AKI30009 Homo
18	1054.4	44.4	1687	9 BC007855 Homo
19	1034.2	43.6	2176	6 AR16407 Sequence

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_GenSeq_23Sep04:*

1: geneseq19800:*

2: geneseq19900:*

3: geneseq12000:*

4: geneseq20010:*

5: geneseq10010:*

6: geneseq20020:*

7: geneseq20020:*

8: geneseq20030:*

9: geneseq20030:*

10: geneseq20030:*

11: geneseq20030:*

12: geneseq20030:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Maximum DB seq length: 2000000000

Result- No.	Score	Query	Match	Length	DB	ID	Description
1	2374	10.0	2374	2	AAV18253		Aav18253 Bovine gr
2	1467.4	61.8	2039	4	AAE9535		Aaf80535 Receptor
3	1467.4	61.8	2039	8	ABX77516		Abx77516 Human Different
4	1467.4	61.8	2039	12	ADL12749		Adl12749 Human stc
5	1399.6	59.0	1920	2	AAZ28653		Aaz28653 Nucleotid
6	1399.6	59.0	1920	3	AAZ40573		Aaz40573 Xenopus b
7	1384.6	58.3	1909	2	AAV13101		Aav13101 Human hsf
8	1384.6	58.3	1909	6	ABL61945		Abl61945 Colon ade
9	1384.6	58.3	1909	6	ABK64750		Abk64750 Human ben
10	1384.6	58.3	1909	10	ADL13671		Adl13671 Osteoarthr
11	1384.6	58.3	1909	12	ADG20468		Adg20468 Human Frz
12	1384.6	58.3	1909	12	ADP21354		Adp21354 Gene FRZB
13	1376.4	58.0	1893	2	AAV14017		Aav14017 Human "fr
14	1124.4	47.3	1484	2	AAV18254		Aav18254 Human gro
15	1122.8	47.3	1476	8	AAD52561		Ad52561 FRZB DNA.
16	1122.8	47.3	1476	8	ABZ201833		Abz201833 SAR-2 nu
17	1122.8	47.3	1476	10	ADK66946		Adk66946 Gene #36
18	1122.8	47.3	1476	10	ADG20470		Adg20470 Mouse Frz
19	1070	45.1	2540	12	ADG20470		Aav14016 Mouse "fr
20	1034.2	43.6	2176	2	AAV14016		Aav14016 Mouse "fr
21	1034.2	43.6	2176	6	AB199691		Ab199691 Mouse isc
22	858	36.1	978	10	ADL13672		Adl13672 Osteoarthr
23	831.8	30.0	1786	2	AAV13102		Aav13102 Mouse hsf
24	831.8	35.0	2441	2	AAV13104		Aav13104 Mouse hsf
25	607.2	25.6	1076	2	AAV13100		Aav13100 Hamster B
26	452	19.0	1291	2	AAV18255		Aav18255 Xenopus g
27	446	18.8	1875	2	AAV14014		Aav14014 Xenopus "
28	424.6	17.9	5301	2	AAV13105		Aav13105 Mouse hsf
29	424.6	17.9	5355	2	AAV13103		Aav13103 Mouse hsf
30	394	16.6	3964	9	ACH13647		Ach13647 Human adu
31	313.4	13.2	1041	3	AAK99046		Aak99046 Bos tauru
32	310.2	13.1	1046	2	AAK28655		Aax28655 Nucleotid
33	310.2	13.1	1581	2	AAK28656		Aax28656 Full leng
34	310.2	13.1	1767	4	AAK84495		Aak84495 Human FRA
35	308.6	13.0	1458	2	AAV08951		Aav08951 Human ATG
36	308.6	13.0	1767	2	AAV80657		Aav80657 Human FRA
37	308.6	13.0	1988	9	ADZ24512		Adz24512 Human cDN
38	308.6	13.0	2009	4	AAF80598		Aaf80598 Receptor
39	306.4	12.9	2819	8	ADZ5271		Adz5271 SRFP 4 DN
40	305.4	12.9	1041	3	AAK54128		Aak54128 Breast ca
41	305.4	12.9	2820	6	ABK322118		Abk322118 Prostate
42	305.4	12.9	2820	8	ABZ234846		Abz234846 Coding se
43	305.4	12.9	2820	8	ABX76341		Abx76341 Lung canc
44	305.4	12.9	2820	8	ABK75341		Abk75341 Human cDN
45	305.4	12.9	2820	8	ABZ201843		Abz201843 SRFP-1 nu

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued_Patents_NA.*:
1: /cgn2_6/ptodata/1/ina/5A_COMBO.seq:/*
2: /cgn2_6/ptodata/1/ina/5B_COMBO.seq:/*
3: /cgn2_6/ptodata/1/ina/6A_COMBO.seq:/*
4: /cgn2_6/ptodata/1/ina/6B_COMBO.seq:/*
5: /cgn2_6/ptodata/1/ina/PCFTUS_COMBO.seq:/*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result- No.	Score	Query	Match	Length	DB	ID	Description
1	2374	10.0	2374	2	AAV18253		Aav18253 Bovine gr
2	1467.4	61.8	2039	4	AAE9535		Aaf80535 Receptor
3	1467.4	61.8	2039	8	ABX77516		Abx77516 Human Different
4	1467.4	61.8	2039	12	ADL12749		Adl12749 Human stc
5	1399.6	59.0	1920	2	AAZ28653		Aaz28653 Nucleotid
6	1399.6	59.0	1920	3	AAZ40573		Aaz40573 Xenopus b
7	1384.6	58.3	1909	2	AAV13101		Aav13101 Human hsf
8	1384.6	58.3	1909	6	ABL61945		Abl61945 Colon ade
9	1384.6	58.3	1909	6	ABK64750		Abk64750 Human ben
10	1384.6	58.3	1909	10	ADL13671		Adl13671 Osteoarthr
11	1384.6	58.3	1909	12	ADG20468		Adg20468 Human Frz
12	1384.6	58.3	1909	12	ADP21354		Adp21354 Gene FRZB
13	1376.4	58.0	1893	2	AAV14017		Aav14017 Human "fr
14	1124.4	47.3	1484	2	AAV18254		Aav18254 Human gro
15	1122.8	47.3	1476	8	AAD52561		Ad52561 FRZB DNA.
16	1122.8	47.3	1476	8	ABZ201833		Abz201833 SAR-2 nu
17	1122.8	47.3	1476	10	ADK66946		Adk66946 Gene #36
18	1122.8	47.3	1476	10	ADG20470		Adg20470 Mouse Frz
19	1070	45.1	2540	12	ADG20470		Aav14016 Mouse "fr
20	1034.2	43.6	2176	2	AAV14016		Aav14016 Mouse "fr
21	1034.2	43.6	2176	6	AB199691		Ab199691 Mouse isc
22	858	36.1	978	10	ADL13672		Adl13672 Osteoarthr
23	831.8	30.0	1786	2	AAV13102		Aav13102 Mouse hsf
24	831.8	35.0	2441	2	AAV13104		Aav13104 Mouse hsf
25	607.2	25.6	1076	2	AAV13100		Aav13100 Hamster B
26	452	19.0	1291	2	AAV18255		Aav18255 Xenopus g
27	446	18.8	1875	2	AAV14014		Aav14014 Xenopus "
28	424.6	17.9	5301	2	AAV13105		Aav13105 Mouse hsf
29	424.6	17.9	5355	2	AAV13103		Aav13103 Mouse hsf
30	394	16.6	3964	9	ACH13647		Ach13647 Human adu
31	313.4	13.2	1041	3	AAK99046		Aak99046 Bos tauru
32	310.2	13.1	1046	2	AAK28655		Aax28655 Nucleotid
33	310.2	13.1	1581	2	AAK28656		Aax28656 Full leng
34	310.2	13.1	1767	4	AAK84495		Aak84495 Human FRA
35	308.6	13.0	1458	2	AAV08951		Aav08951 Human ATG
36	308.6	13.0	1767	2	AAV80657		Aav80657 Human FRA
37	308.6	13.0	1988	9	ADZ24512		Adz24512 Human cDN
38	308.6	13.0	2009	4	AAF80598		Aaf80598 Receptor
39	306.4	12.9	2819	8	ADZ5271		Adz5271 SRFP 4 DN
40	305.4	12.9	1041	3	AAK54128		Aak54128 Breast ca
41	305.4	12.9	2820	6	ABK322118		Abk322118 Prostate
42	305.4	12.9	2820	8	ABZ234846		Abz234846 Coding se
43	305.4	12.9	2820	8	ABX76341		Abx76341 Lung canc
44	305.4	12.9	2820	8	ABK75341		Abk75341 Human cDN
45	305.4	12.9	2820	8	ABZ201843		Abz201843 SRFP-1 nu

Result- No.	Score	Query	Match	Length	DB	ID	Description
1	1467.4	61.8	2039	3	US-09-276-531-45		Sequence 45, Appl
2	1467.4	61.8	2039	4	US-09-976-594-478		Sequence 478, Appl
3	1376.4	58.0	1893	3	US-08-870-474-10		Sequence 10, Appl
4	1034.2	43.6	2176	3	US-08-878-474-8		Sequence 8, Appl
5	858	36.1	1886	2	US-08-878-484-2		Sequence 277, Appl
6	308.6	13.0	2009	3	US-09-276-531-108		Sequence 277, Appl
7	209.4	8.8	246	4	US-09-016-434-103		Sequence 103, Appl
8	72	3.0	401	4	US-09-564-940B-277		Sequence 277, Appl
9	72	3.0	401	4	US-09-546-943-10		Sequence 5, Appl
10	72	3.0	401	4	US-09-546-943-11		Sequence 277, Appl
11	72	3.0	401	4	US-09-546-943-12		Sequence 277, Appl
12	58.4	2.5	942	4	US-09-546-943-2		Sequence 2, Appl
13	58.4	2.5	1017	4	US-09-546-943-9		Sequence 9, Appl
14	58.4	2.5	2075	4	US-09-087-031R-2		Sequence 2, Appl
15	58.4	2.5	2075	4	US-09-546-943-1		Sequence 1, Appl
16	58.4	2.5	2078	4	US-09-087-031E-1		Sequence 1, Appl
17	58.4	2.5	4245	3	US-09-276-531-16		Sequence 16, Appl
18	58.4	2.5	4500	4	US-09-087-031E-27		Sequence 27, Appl
19	58.4	2.5	1308	4	US-09-937-067-18		Sequence 18, Appl
20	58.4	2.5	1869	4	US-09-148-545-56		Sequence 56, Appl
21	58.4	2.5	870	4	US-09-937-067-3		Sequence 3, Appl
22	54.6	2.3	1960	4	US-09-148-545-114		Sequence 114, Appl
23	54.6	2.3	1141	4	US-09-806-708B-22		Sequence 22, Appl
24	49.4	2.1	7218	1	US-09-232-463-14		Sequence 14, Appl
25	49.4	2.1	2030	4	US-09-937-067-1		Sequence 1, Appl
26	45.2	1.9	2124	4	US-09-087-031E-26		Sequence 26, Appl
27	45.2	1.9	221	4	US-09-621-976-13585		Sequence 1355, A
28	45.2	1.9	1796	3	US-09-276-531-113		Sequence 113, Appl
29	45.2	1.9	2185	4	US-09-360-545-66		Sequence 66, Appl
30	44.4	1.9	1305	4	US-09-815-783-3		Sequence 3, Appl
31	49.2	2.1	2030	4	US-09-157-864-3		Sequence 1, Appl
32	45.2	1.9	2124	4	US-09-087-031E-26		Sequence 26, Appl
33	45.2	1.9	221	4	US-09-621-976-13585		Sequence 1355, A
34	45.2	1.9	1796	3	US-09-276-531-113		Sequence 113, Appl
35	45.2	1.9	2185	4	US-09-360-545-66		Sequence 66, Appl
36	44.4	1.9	1305	4	US-09-815-783-3		Sequence 3, Appl
37	44.4	1.9	1430	4	US-09-157-864-3		Sequence 1, Appl
38	44.2	1.9	1141	4	US-09-806-708B-22		Sequence 22, Appl
39	44.2	1.9	11558	5	PCT-US93-06251-23		Sequence 23, Appl
40	44	1.9	1401	4	US-09-252-991A-14814		Sequence 14814, A
41	44</td						

SUMMARIES

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%
Listing first 45 summaries

Database : GenEmbl:*

CR022855 full-leng

CR020343 full-leng

AK029941 Mus muscu

AK019093 Mus muscu

CR093578 full-leng

AL515416 AL515416

AL528836 AL528836

AL546734 AL546734

AL548498 AL548498

AL5182 U69182 Soar

AL527859 AL527859

CK775692 966826 MA

AL573040 AL573040

AL526385 AL526385

CD05319 AGENCOURT

CR053950 CR453950

AY410028 Homo sapi

B1913036 603179601

B1932471 603082261

AU141161 AU141161

BX459201 BX459201

BP147378 BP147378

BP148017 BP148017

CN315376 170004245

BX055693 DKFZ0781C

B1769191 603000007

BP455757 BP455757

AL526570 AL526570

AY410030 Mus muscu

CF411660 CH3#075_B

AL546699 AL546699

AW160750 aut7561.Y

AY410029 Pan trogl

CN315375 170004246

AL528835 AL528835

B1761532 603046682

BU09451 603157994

BM253949 515238 MA

AU117730 AU117730

BP152493 BP152493

BU852855 AGENCOURT

CA773784 Im57411.Y

BX955707 DKFZ0781D

CB160361 K-EST0220

BM031987 497568 MA

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: January 10, 2005, 11:50:10 ; Search time 6129.68 Seconds
(without alignments)
11448.874 Million cell updates/sec

Score: US-10-028-051A-3
Sequence: 1 cggggctcgccggaggg.....acatgtgtttaaaaaaa 1484
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Title: Perfect score: 1484
Sequence: 1 cggggctcgccggaggg.....acatgtgtttaaaaaaa 1484
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result : GenEmbl:*

CR022855 full-leng

CR020343 full-leng

AK029941 Mus muscu

AK019093 Mus muscu

CR093578 full-leng

AL515416 AL515416

AL528836 AL528836

AL546734 AL546734

AL548498 AL548498

AL5182 U69182 Soar

AL527859 AL527859

CK775692 966826 MA

AL573040 AL573040

AL526385 AL526385

CD05319 AGENCOURT

CR053950 CR453950

AY410028 Homo sapi

B1913036 603179601

B1932471 603082261

AU141161 AU141161

BX459201 BX459201

BP147378 BP147378

BP148017 BP148017

CN315376 170004245

BX055693 DKFZ0781C

B1769191 603000007

BP455757 BP455757

AL526570 AL526570

AY410030 Mus muscu

CF411660 CH3#075_B

AL546699 AL546699

AW160750 aut7561.Y

AY410029 Pan trogl

CN315375 170004246

AL528835 AL528835

B1761532 603046682

BU09451 603157994

BM253949 515238 MA

AU117730 AU117730

BP152493 BP152493

BU852855 AGENCOURT

CA773784 Im57411.Y

BX955707 DKFZ0781D

CB160361 K-EST0220

BM031987 497568 MA

Result

No.

Score

Match

Length

DB

ID

%

Description

Post-processing:

Maximum

Match

0%

Maximum

DB seq

length:

2000000000

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 647.611 Seconds (without alignments) 12029.047 Million cell updates/sec

Title: US-10-028-051A-3

Perfect score: 1484

Sequence: 1 cggggcctgggggggggg.....acatgtgtttaaaaaaaaaa 1484

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1: geneseq1980s:*

2: geneseq1990s:*

3: geneseq2000s:*

4: geneseq2001as:*

5: geneseq2001bs:*

6: geneseq2002as:*

7: geneseq2002bs:*

8: geneseq2003as:*

9: geneseq2003bs:*

10: geneseq2003ds:*

11: geneseq2003ds:*

12: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 130.56 Seconds (without alignments) 8079.143 Million cell updates/sec

Title: US-10-028-051A-3

Perfect score: 1484

Sequence: 1 cggggcctgggggggggg.....acatgtgtttaaaaaaaaaa 1484

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : AA18254 Human gro

1: AA18254 Human gro

2: ABX7532 Human cDN

3: ABX7532 Human cDN

4: ABX7532 Human cDN

5: ABX7532 Human cDN

6: ABX7532 Human cDN

7: ABX7532 Human cDN

8: ABX7532 Human cDN

9: ABX7532 Human cDN

10: ABX7532 Human cDN

11: ABX7532 Human cDN

12: ABX7532 Human cDN

13: ABX7532 Human cDN

14: ABX7532 Human cDN

15: ABX7532 Human cDN

16: ABX7532 Human cDN

17: ABX7532 Human cDN

18: ABX7532 Human cDN

19: ABX7532 Human cDN

20: ABX7532 Human cDN

21: ABX7532 Human cDN

22: ABX7532 Human cDN

23: ABX7532 Human cDN

24: ABX7532 Human cDN

25: ABX7532 Human cDN

26: ABX7532 Human cDN

27: ABX7532 Human cDN

28: ABX7532 Human cDN

29: ABX7532 Human cDN

30: ABX7532 Human cDN

31: ABX7532 Human cDN

32: ABX7532 Human cDN

33: ABX7532 Human cDN

34: ABX7532 Human cDN

35: ABX7532 Human cDN

36: ABX7532 Human cDN

37: ABX7532 Human cDN

38: ABX7532 Human cDN

39: ABX7532 Human cDN

40: ABX7532 Human cDN

41: ABX7532 Human cDN

42: ABX7532 Human cDN

43: ABX7532 Human cDN

44: ABX7532 Human cDN

45: ABX7532 Human cDN

17: AA134.6 88.6 1909 12 ADP21354

18: AA134.6 75.8 2374 2 AAV18253

19: AA134.6 65.8 978 10 ADL13672

20: AA134.6 57.0 2540 12 ADG20470

21: AA134.6 56.9 2441 2 AAV13104

22: AA134.6 56.8 1785 2 AAV13102

23: AA134.6 56.1 2176 2 AAV14016

24: AA134.6 56.1 2176 6 ADI99691

25: AA134.6 42.5 1076 2 AAV13100

26: AA134.6 31.7 476 6 ABK46764

27: AA134.6 31.4 1291 2 AAV18255

28: AA134.6 31.1 1874 2 AAV14014

29: AA134.6 29.4 475 9 ACH13647

30: AA134.6 28.3 5301 2 AAV13105

31: AA134.6 28.3 5355 2 AAV13103

32: AA134.6 27.4 489 9 ACH18855

33: AA134.6 19.7 1041 3 AAV19046

34: AA134.6 19.5 1458 2 AAV08951

35: AA134.6 19.5 1988 9 ADA24512

36: AA134.6 19.5 2009 4 AAF0598

37: AA134.6 19.5 2819 8 AAD2571

38: AA134.6 19.4 1045 2 AAX18655

39: AA134.6 19.4 1581 2 AAX18656

40: AA134.6 19.4 1757 4 AAC84495

41: AA134.6 19.3 1041 3 AAS54128

42: AA134.6 19.3 1767 2 AAV0657

43: AA134.6 19.3 2820 6 ABK93118

44: AA134.6 19.3 2820 8 ABZ34846

45: AA134.6 19.3 2820 8 ABZ34841

BV158572 REAMMSEQ00

Aut009304 Xenopus 1

AC126647 Rattus no

CQ695880 Sequence

AC105396 Homo sapi

AAV13102 Mouse hsf

AAV14016 Mouse "fr

AAV18253 Bovine gr

ADL13672 Osteoearth

ADG20470 Mouse Fri

AAV13104 Mouse hsf

AAV13102 Mouse hsf

AAV14014 Xenopus "

Ach13647 Human adu

Aav13105 Mouse hsf

Aav13100 Hamster B

Ak64764 Human ben

Aav18255 Xenopus g

Aav14014 Xenopus "

Ach13647 Human adu

Aav13105 Mouse hsf

Aav13100 Hamster B

Ach18855 Human adu

Aad9046 Bos tauru

Aav08951 Human ATG

Ad24512 Human CDN

Aaf0598 Receptor

Ad152571 SRFP 4 DN

Aax18655 Nucleotid

Aax18656 Full leng

Aac84495 Human FRA

Aas54128 Breast ca

Aav0657 Human FRA

Abx92118 Prostate

Abx34846 Coding se

Abx76341 Lung canc

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 130.56 Seconds (without alignments) 8079.143 Million cell updates/sec

Title: US-10-028-051A-3

Perfect score: 1484

Sequence: 1 cggggcctgggggggggg.....acatgtgtttaaaaaaaaaa 1484

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/pctodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/pctodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/pctodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/pctodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/pctodata/1/ina/PTTUS_COMB.seq:*

6: /cgn2_6/pctodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 130.56 Seconds (without alignments) 8079.143 Million cell updates/sec

Title: US-10-028-051A-3

Perfect score: 1484

Sequence: 1 cggggcctgggggggggg.....acatgtgtttaaaaaaaaaa 1484

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/pctodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/pctodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/pctodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/pctodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/pctodata/1/ina/PTTUS_COMB.seq:*

6: /cgn2_6/pctodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 130.56 Seconds (without alignments) 8079.143 Million cell updates/sec

Title: US-10-028-051A-3

Perfect score: 1484

Sequence: 1 cggggcctgggggggggg.....acatgtgtttaaaaaaaaaa 1484

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/pctodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/pctodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/pctodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/pctodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/pctodata/1/ina/PTTUS_COMB.seq:*

6: /cgn2_6/pctodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 130.56 Seconds (without alignments) 8079.143 Million cell updates/sec

Title: US-10-028-051A-3

Perfect score: 1484

Sequence: 1 cggggcctgggggggggg.....acatgtgtttaaaaaaaaaa 1484

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/pctodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/pctodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/pctodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/pctodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/pctodata/1/ina/PTTUS_COMB.seq:*

6: /cgn2_6/pctodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 130.56 Seconds (without alignments) 8079.143 Million cell updates/sec

Title: US-10-028-051A-3

Perfect score: 1484

Sequence: 1 cggggcctgggggggggg.....acatgtgtttaaaaaaaaaa 1484

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/pctodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/pctodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/pctodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/pctodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/pctodata/1/ina/PTTUS_COMB.seq:*

6: /cgn2_6/pctodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 130.56 Seconds (without alignments) 8079.143 Million cell updates/sec

Title: US-10-028-051A-3

Perfect score: 1484

Sequence: 1 cggggcctgggggggggg.....acatgtgtttaaaaaaaaaa 1484

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/pctodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/pctodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/pctodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/pctodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/pctodata/1/ina/PTTUS_COMB.seq:*

6: /cgn2_6/pctodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match Length	DB	ID	Description	
1	1464.4	98.7	2039	3	US-09-276-531-45	
2	1464.4	98.7	2039	4	US-09-976-594-478	
3	1316.2	88.7	1893	3	US-08-878-474-10	
4	832.8	56.1	2176	3	US-08-878-474-8	
5	462	31.1	1875	3	US-08-878-474-4	
6	289.4	19.5	2009	3	US-03-676-531-108	
7	235	15.8	246	4	US-09-016-434-103	
8	64	4.3	401	4	US-09-643-597-277	
9	64	4.3	401	4	US-09-648-884A-277	
10	64	4.3	401	4	US-09-642-613A-277	
11	64	4.3	401	4	US-09-606-21B-277	
12	64	4.3	401	4	US-09-630-940B-277	
13	61.4	4.1	588	4	US-09-546-043-10	
14	61.4	4.1	1984	4	US-08-937-067-4	
15	59	4.0	741	4	US-09-546-043-11	
16	59	4.0	804	4	US-09-546-043-12	
17	59	4.0	942	4	US-09-546-043-2	
18	59	4.0	1017	4	US-09-546-043-9	
19	59	4.0	2075	4	US-09-087-031E-27	
20	59	4.0	2075	4	US-09-546-043-1	
21	59	4.0	2075	4	US-09-514-885-2	
22	59	4.0	2078	4	US-09-087-031E-1	
23	59	4.0	4245	4	US-09-276-531-16	
24	59	4.0	4500	4	US-09-087-031E-27	
25	57.4	3.9	1308	4	US-08-937-067-18	
26	51.8	3.5	1869	4	US-09-148-545-56	
27	51.2	3.5	870	4	US-08-937-067-3	
28	51.2	3.5	1960	4	US-09-148-545-14	
29	49	3.3	2030	4	US-08-937-067-1	
30	46.8	3.2	6090	4	US-09-631-603-1	
31	45.8	3.1	7218	4	US-08-232-463-14	
32	45.2	3.0	546	4	US-09-252-991A-6912	
c	33	45.2	3.0	1197	4	US-09-252-991A-6737
c	34	45.2	3.0	1272	4	US-09-252-991A-6952
c	35	45.2	3.0	2346	4	US-09-252-991A-6782
c	36	44.6	3.0	2124	4	US-09-087-031E-6
c	37	43	2.9	711	4	US-09-252-991A-5727
c	38	43	2.9	765	4	US-09-252-991A-15854
c	39	43	2.9	1548	4	US-09-252-991A-5713
c	40	43	2.9	1971	4	US-09-252-991A-5699
c	41	43	2.9	2265	4	US-09-252-991A-5738
c	42	42.8	2.9	2310	3	US-08-956-182-13
c	43	42.8	2.9	7218	1	US-08-232-463-14
c	44	42.4	2.9	1449	4	US-09-252-991A-10586
c	45	42.4	2.9	3222	4	US-09-252-991A-10770
OM nucleic - nucleic search, using aw model						
Copyright (c) 1993 - 2005 Compugen Ltd.						
Run on: January 10, 2005, 11:50:10 ; Search time 1411.66 Seconds						
(without alignments)						
6031.844 Million cell updates/sec						
Title: US-10-028-051A-3						
Perfect score: 1484						
Sequence: 1 cggggcctgggggggggg.....acatgtgtttaaaaaaaaa 1484						
Scoring table: IDENTITY_NUC						
Searched: GapOp 10.0 , GapExt 1.0						
Total number of hits satisfying chosen parameters: 8586996						
Minimum DB seq length: 0						
Maximum DB seq length: 200000000						
Post-processing: Minimum Match 0%						
Database :						
Published_Applications_NA:*						
1:	/cgn2_6/ptodata/1/pupna/US07_PUBCOMB.seq:*					
2:	/cgn2_6/ptodata/1/pupna/PCT_NEW_PUB.seq:*					
3:	/cgn2_6/ptodata/1/pupna/US06_NEW_PUB.seq:*					
4:	/cgn2_6/ptodata/1/pupna/US06_PUBCOMB.seq:*					
5:	/cgn2_6/ptodata/1/pupna/US07_NEW_PUB.seq:*					
6:	/cgn2_6/ptodata/1/pupna/PCTUS_PUBCOMB.seq:*					
7:	/cgn2_6/ptodata/1/pupna/US08_NEW_PUB.seq:*					
8:	/cgn2_6/ptodata/1/pupna/US08_PUBCOMB.seq:*					
9:	/cgn2_6/ptodata/1/pupna/US09A_PUBCOMB.seq:*					
10:	/cgn2_6/ptodata/1/pupna/US09B_PUBCOMB.seq:*					
11:	/cgn2_6/ptodata/1/pupna/US09C_PUBCOMB.seq:*					
12:	/cgn2_6/ptodata/1/pupna/US10_E_PUBCOMB.seq:*					
13:	/cgn2_6/ptodata/1/pupna/US10A_PUBCOMB.seq:*					
14:	/cgn2_6/ptodata/1/pupna/US10B_PUBCOMB.seq:*					
15:	/cgn2_6/ptodata/1/pupna/US10C_PUBCOMB.seq:*					
16:	/cgn2_6/ptodata/1/pupna/US10D_PUBCOMB.seq:*					
17:	/cgn2_6/ptodata/1/pupna/US10_E_PUBCOMB.seq:*					
18:	/cgn2_6/ptodata/1/pupna/US10_E_NEW_PUB.seq:*					
19:	/cgn2_6/ptodata/1/pupna/US11_NEW_PUB.seq:*					
20:	/cgn2_6/ptodata/1/pupna/US60_NEW_PUB.seq:*					
21:	/cgn2_6/ptodata/1/pupna/us60_PUBCOMB.seq:*					
SUMMARIES						
Maximum Match 100% Listing first 45 summaries						
Result						
No.	Score	Query	Match Length	DB	ID	

1	1483.6	100.0	1484	13	US-10-028-051-3	
2	1483.6	100.0	1484	14	US-10-020-051-3	
3	1483.6	100.0	1484	15	US-10-014-055-3	
4	1473	99.3	1476	15	US-10-172-118-614	
5	1473	99.3	1476	16	US-10-342-887-614	
6	1464.4	98.7	2039	9	US-09-974-298-16	
7	1472	96.2	2025	16	US-10-062-674-1395	
8	1316.2	88.7	1893	9	US-09-903-180B-10	
9	1316.2	88.7	1893	9	US-09-903-187B-10	
10	1316.2	88.7	1893	9	US-09-903-17A-10	
11	1316.2	88.7	1893	9	US-09-903-188A-10	
12	1316.2	88.7	1893	9	US-09-903-323A-10	
13	1316.2	88.7	1893	9	US-09-903-325A-10	
14	1316.2	88.7	1893	9	US-09-903-317B-10	
15	1314.6	88.6	1909	10	US-09-873-319-645	
16	1314.6	88.6	1909	10	US-09-873-319-645	
17	1314.6	88.6	1909	10	US-09-873-367C-282	
18	1124.4	75.8	2374	13	US-10-028-051-1	
19	1124.4	75.8	2374	14	US-10-090-049-1	
20	1124.4	75.8	2374	15	US-10-014-055-1	
21	832.8	56.1	2176	9	US-09-903-180B-8	
22	832.8	56.1	2176	9	US-09-903-187B-8	
23	832.8	56.1	2176	9	US-09-903-171A-8	
24	832.8	56.1	2176	9	US-09-903-188A-8	
25	832.8	56.1	2176	9	US-09-903-233A-8	
26	832.8	56.1	2176	9	US-09-903-225A-8	
27	832.8	56.1	2176	9	US-09-903-170C-8	
28	832.8	56.1	2176	9	US-09-903-170C-8	
29	483.4	32.6	487	16	US-10-085-782A-36336	
c	30	470.2	31.1	476	10	US-09-960-705-1006
c	31	470.2	31.1	476	10	US-09-987-319-659
c	32	466.4	31.4	1291	13	US-10-028-051-23
c	33	466.4	31.4	1291	14	US-10-030-048-23
c	34	466.4	31.4	1291	15	US-10-014-055-23
c	35	462	31.1	1875	9	US-09-903-180B-4
c	36	462	31.1	1875	9	US-09-903-187A-4
c	37	462	31.1	1875	9	US-09-903-17A-4
c	38	462	31.1	1875	9	US-09-903-188A-4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	
1	1291	10.0	1291	5	XJU78598		U78598 Xenopus lae	
2	1131.6	87.7	1875	5	U68059		U68059 Xenopus lae	
3	1131.6	87.7	1875	6	AR116405		AR116405 Sequence	
4	1131.6	87.7	1875	6	BD195145		BD195145 Endoderm,	
5	1028.2	79.6	1867	5	BC074538		BC074538 Xenopus t	
6	992.4	76.9	1434	5	XLAJ9304		XLAJ9304 Xenopus t	
7	8	40.1	1833	5	AP218057		AP218057 Gallus ga	
8	468	36.3	1920	6	BD192740		BD192740 Secreted	
9	466.4	36.1	1363	9	BC027855		BC027855 Homo sapi	
10	466.4	36.1	1893	6	AR116408		AR116408 Sequence	
11	466.4	36.1	1893	6	BD195148		BD195148 Endoderm,	
12	466.4	36.1	1893	9	HSU68057		HSU68057 Human frezz	
13	466.4	36.1	2039	6	AR129187		AR129187 Sequence	
14	466.4	36.1	2039	6	AR447852		AR447852 Sequence	
15	466.4	36.1	4612	6	AX565712		AX565712 Sequence	
16	464.8	36.0	1476	6	AX397112		AX397112 sequence	
17	464.8	36.0	1476	6	AX701367		AX701367 Sequence	
18	464.8	36.0	1476	6	AX821908		AX821908 Sequence	
19	464.8	36.0	1476	9	HSU24163		HSU24163 Human Frizz	
20	464.8	36.0	1909	6	AX329773		AX329773 Sequence	
21	464.8	36.0	1909	9	HSU91903		U91903 Human Fritz	
22	463.6	35.9	2814	10	BC016884		BC016884 Mus muscu	
23	462	35.8	2176	6	AR116407		AR116407 Sequence	
24	462	35.8	2176	6	BD195147		BD195147 Endoderm,	
25	462	35.8	2176	6	AX305981		AX305981 Sequence	
26	462	35.8	2176	6	U68058		U68058 Mus musculu	
27	462	35.8	2176	10	MMU85568		U88568 Mus musculu	
28	462	35.8	2540	10	AKI3009		U84164 Bos taurus	
29	452	35.0	2351	4	BTWU24164		AF116853 Danio rer	
30	394.6	30.6	948	5	AF116853		U91904 Mesocricetus	
31	373.6	28.9	1076	10	MAU91904		AF207665 Gallus ga	
32	373.4	28.9	640	5	ACI08514		ACI08514 Homo sapi	
33	345.6	26.8	725	6	AL928578		AL928578 Mouse DNA	
34	283.6	22.0	1687	9	CO719712		ACI26647 Rattus no	
35	266.6	17.85	10	1785	10	AKI3009		ACI34905 Mus muscu
36	263.4	20.4	1739	10	BC034653		BC034653 Mus muscu	
37	259.8	20.1	97944	9	ACI08514		ACI08514 Homo sapi	
38	258.6	20.0	190806	10	AL928578		AL928578 Mouse DNA	
39	258.6	20.0	23965	2	ACI26647		ACI26647 Rattus no	
40	258.6	20.0	250663	2	ACI34905		ACI34905 Mus muscu	
41	257.2	19.9	611	11	BV099134		BV099134 RPLAMMSQO	
42	257.2	19.9	611	11	BV158572		BV158572 RPLAMMSQO	
43	251.8	19.5	1910	10	AF012891		AF012891 Rattus no	
44	250.8	19.4	1715	10	AF140346		AF140346 Rattus no	
45	247.6	19.2	162126	2	CRS13785		CRS13785 Danio rer	

GenCore version 5.1-6

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OM nucleic - nucleic search, using sw model

Run on : January 10, 2005, 11:50:10 ; Search time 563.386 Seconds

(without alignments)

12029.047 Million cell updates/sec

Title: US-10-028-051A-23
Perfect score: 1291
Sequence: ttactgtggcagtttcccc.....agccatcatcattgtatca 1291

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134866 seqB, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772
Minimum DB seq length: 0
Maximum DB seq length: 200000000

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	
1	1291	10.0	1291	5	XJU78598		U78598 Xenopus lae	
2	1131.6	87.7	1875	5	U68059		U68059 Xenopus lae	
3	1131.6	87.7	1875	6	AR116405		AR116405 Sequence	
4	1131.6	87.7	1875	6	BD195145		BD195145 Endoderm,	
5	1028.2	79.6	1867	5	BC074538		BC074538 Xenopus t	
6	992.4	76.9	1434	5	XLAJ9304		XLAJ9304 Xenopus t	
7	8	40.1	1833	5	AP218057		AP218057 Gallus ga	
8	468	36.3	1920	6	BD192740		BD192740 Secreted	
9	466.4	36.1	1363	9	BC027855		BC027855 Homo sapi	
10	466.4	36.1	1893	6	AR116408		AR116408 Sequence	
11	466.4	36.1	1893	6	BD195148		BD195148 Endoderm,	
12	466.4	36.1	1893	9	HSU68057		HSU68057 Human frezz	
13	466.4	36.1	2039	6	AR129187		AR129187 Sequence	
14	466.4	36.1	2039	6	AR447852		AR447852 Sequence	
15	466.4	36.1	4612	6	AX565712		AX565712 Sequence	
16	464.8	36.0	1476	6	AX397112		AX397112 sequence	
17	464.8	36.0	1476	6	AX701367		AX701367 Sequence	
18	464.8	36.0	1476	6	AX821908		AX821908 Sequence	
19	464.8	36.0	1476	9	HSU24163		HSU24163 Human Frizz	
20	464.8	36.0	1909	6	AX329773		AX329773 Sequence	
21	464.8	36.0	1909	9	HSU91903		U91903 Human Fritz	
22	463.6	35.9	2814	10	BC016884		BC016884 Mus muscu	
23	462	35.8	2176	6	AR116407		AR116407 Sequence	
24	462	35.8	2176	6	BD195147		BD195147 Endoderm,	
25	462	35.8	2176	6	AX305981		AX305981 Sequence	
26	462	35.8	2176	6	U68058		U68058 Mus musculu	
27	462	35.8	2176	10	MMU85568		U88568 Mus musculu	
28	462	35.8	2540	10	AKI3009		U84164 Bos taurus	
29	452	35.0	2351	4	BTWU24164		AF116853 Danio rer	
30	394.6	30.6	948	5	AF116853		U91904 Mesocricetus	
31	373.6	28.9	1076	10	MAU91904		AF207665 Gallus ga	
32	373.4	28.9	640	5	ACI08514		ACI08514 Homo sapi	
33	345.6	26.8	725	6	AL928578		AL928578 Mouse DNA	
34	283.6	22.0	1687	9	CO719712		ACI26647 Rattus no	
35	266.6	17.85	10	1785	10	AKI3009		ACI34905 Mus muscu
36	263.4	20.4	1739	10	BC034653		BC034653 Mus muscu	
37	259.8	20.1	97944	9	ACI08514		ACI08514 Homo sapi	
38	258.6	20.0	190806	10	AL928578		AL928578 Mouse DNA	
39	258.6	20.0	23965	2	ACI26647		ACI26647 Rattus no	
40	258.6	20.0	250663	2	ACI34905		ACI34905 Mus muscu	
41	257.2	19.9	611	11	BV099134		BV099134 RPLAMMSQO	
42	257.2	19.9	611	11	BV158572		BV158572 RPLAMMSQO	
43	251.8	19.5	1910	10	AF012891		AF012891 Rattus no	
44	250.8	19.4	1715	10	AF140346		AF140346 Rattus no	
45	247.6	19.2	162126	2	CRS13785		CRS13785 Danio rer	

SUMMARIES

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1	1291	10.0	1291	2	AAV13104		AAV13104 Mouse hsc
2	462	35.8	2540	12	ADG20470		ADG20470 Mouse Fri
3	452.8	35.6	978	10	ADL13672		ADL13672 Osteoarthritis
4	452.8	35.6	978	10	AAV18253		AAV18253 Bovine gr
5	452.8	35.6	2374	2	AAV18253		AAV18253 Bovine gr
6	452.8	35.6	2374	2	AAV18253		AAV18253 Bovine gr
7	373.6	28.9	1076	2	AAV13100		AAV13100 Hamster gr
8	321.6	24.9	352	3	AAK43168		Aak43168 Xenopus a
9	245.8	19.0	5301	2	AAV13105		Aav13105 Mouse hsf
10	245.8	19.0	5355	2	AAV13103		Aav13103 Mouse hsf
11	244.2	18.9	1458	2	AAV08951		Aav08951 Human ATG
12	244.2	18.9	1988	9	ADA24512		Ada24512 Human cDN
13	244.2	18.9	2009	4	AAF0598		Aaf0598 Receptor
14	241	18.7	1041	3	AAC5128		Aaa5128 Breast ca
15	241	18.7	1045	2	AAX8655		Aax8655 Nucleotide
16	241	18.7	1581	2	AAX8656		Aax8656 Full leng
17	241	18.7	1767	2	AAV0657		Aav0657 Human FRA
18	241	18.7	1767	4	AAC84495		Aac84495 Human FRA
19	241	18.7	2820	6	ABK2118		Abk2118 Prostate
20	241	18.7	2820	8	ABZ34846		Abz34846 Coding se

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB ID	Description
1	1291	100.0 1291 13 US-10-028-051-23	Sequence 23, Appl
2	1291	100.0 1291 14 US-10-020-049-23	Sequence 23, Appl
3	1291	100.0 1291 15 US-10-014-055-23	Sequence 23, Appl
4	1131.6	87.7 1875 9 US-09-903-180B-4	Sequence 4, Appl
5	1131.6	87.7 1875 9 US-09-903-187A-4	Sequence 4, Appl
6	1131.6	87.7 1875 9 US-09-903-171A-4	Sequence 4, Appl
7	1131.6	87.7 1875 9 US-09-903-188A-4	Sequence 4, Appl
8	1131.6	87.7 1875 9 US-09-903-323A-4	Sequence 4, Appl
9	1131.6	87.7 1875 9 US-09-903-325A-4	Sequence 4, Appl
10	1131.6	87.7 1875 9 US-09-903-170C-4	Sequence 4, Appl
11	466.4	36.1 1484 13 US-10-028-051-3	Sequence 3, Appl
12	466.4	36.1 1484 14 US-10-020-049-3	Sequence 3, Appl
13	466.4	36.1 1893 9 US-10-014-055-3	Sequence 3, Appl
14	466.4	36.1 1893 9 US-09-903-180B-10	Sequence 10, Appl
15	466.4	36.1 1893 9 US-09-903-187A-10	Sequence 10, Appl
16	466.4	36.1 1893 9 US-09-903-171A-10	Sequence 10, Appl
17	466.4	36.1 1893 9 US-09-903-188A-10	Sequence 10, Appl
18	466.4	36.1 1893 9 US-09-903-323A-10	Sequence 10, Appl
19	466.4	36.1 1893 9 US-09-903-325A-10	Sequence 10, Appl
20	466.4	36.1 1893 9 US-09-903-170C-10	Sequence 10, Appl
21	466.4	36.1 2039 9 US-09-970-298-16	Sequence 16, Appl
22	466.4	36.1 2825 16 US-10-062-674-1395	Sequence 1395, Appl
23	464.8	36.0 1476 15 US-10-172-118-614	Sequence 614, Appl
24	464.8	36.0 1476 16 US-10-342-887-614	Sequence 614, Appl
25	464.8	36.0 1909 10 US-09-960-706-989	Sequence 989, Appl
26	464.8	36.0 1909 10 US-09-873-319-645	Sequence 645, Appl
27	464.8	36.0 1909 10 US-09-873-367C-282	Sequence 282, Appl
28	462	35.8 2176 9 US-09-903-180B-8	Sequence 8, Appl
29	462	35.8 2176 9 US-09-903-187A-8	Sequence 8, Appl
30	462	35.8 2176 9 US-09-903-171A-8	Sequence 8, Appl
31	462	35.8 2176 9 US-09-903-188A-8	Sequence 8, Appl
32	462	35.8 2176 9 US-09-903-323A-8	Sequence 8, Appl
33	462	35.8 2176 9 US-09-903-325A-8	Sequence 8, Appl
34	462	35.8 2176 9 US-09-903-170C-8	Sequence 8, Appl
35	452	35.0 2374 13 US-10-028-051-1	Sequence 1, Appl
36	452	35.0 2374 14 US-10-030-049-1	Sequence 1, Appl
37	452	35.0 2374 15 US-10-014-055-1	Sequence 1, Appl
38	244.2	18.9 188 14 US-10-208-408-28	Sequence 28, Appl
39	241	18.7 143 16 US-10-610-917-1	Sequence 1, Appl
40	241	18.7 1581 16 US-10-610-917-3	Sequence 3, Appl
41	241	18.7 1581 16 US-10-301-822-188	Sequence 188, Appl
42	241	18.7 2820 15 US-10-295-027-63	Sequence 63, Appl
43	241	18.7 2820 15 US-10-295-027-66	Sequence 960, Appl
44	241	18.7 2820 18 US-10-473-974-204	Sequence 204, Appl
45	241	18.7 2839 9 US-09-909-775-1	Sequence 1, Appl

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OM nucleic - nucleic search, using nw model

Run on: January 10, 2005, 11:50:10 ; Search time 3683.7 Seconds
(without alignments)

12770.772 Million cell updates/sec

Title: US-10-028-051A-23
Perfect score: 1291

Sequence: tttactgtgcagtttccc.....agctatcatcatgtacta 1291

Scoring table: IDENTITY_NUC
gapop 10.0 , Gapext 1.0
Searched: 32822875 seqs, 18219865908 residues
Total number of hits satisfying chosen parameters: 65645750

SUMMARIES

SUMMARIES

Result No.	Score	Query Match Length DB ID	Description
1	770.6	59.7 851 5 BU908005	BU908005 AGENCOURT
2	698.6	54.1 885 6 CA98226 AGENCOURT	CA98226 AGENCOURT
3	662.6	51.3 923 5 BU906569 AGENCOURT	BU906569 AGENCOURT
4	592.2	45.9 702 5 BX853989 BX853989	BX853989 BX853989
5	524.4	40.6 745 6 CF284632 CF284632	CF284632 AGENCOURT
6	495.2	38.4 736 7 CK633921 CK633921	CK633921 AGENCOURT
7	480.6	37.2 929 5 BX755490 BX755490	BX755490 BX755490
8	466.4	36.1 1305 3 CR593578 CR593578	CR593578 full-leng
9	466.4	36.1 1780 3 CR620343 CR620343	CR620343 full-leng
10	466.4	36.1 1891 3 CR628555 CR628555	CR628555 full-leng
11	462	35.8 2390 3 AK01093 AK01093	AK01093 Mus muscu
12	462	35.8 2922 3 AK029941 AK029941	AK029941 Mus muscu
13	453.6	35.1 1001 1 AL548498 AL548498	AL548498 AL548498
14	451.4	35.0 1032 1 AL546734 AL546734	AL546734 AL546734
15	447.6	34.7 1159 1 AL51416 AL51416	AL51416 AL51416
16	446.6	34.6 940 5 BU40451 BU40451	BU40451 60317994
17	434.6	33.7 882 5 BX758011 BX758011	BX758011 BX758011
18	330.9	33.3 891 6 CD105319 CD105319	CD105319 AGENCOURT
19	423.4	32.8 1094 1 AL528836 AL528836	AL528836 AL528836
20	418.2	32.4 835 5 BU910785 BU910785	BU910785 AGENCOURT
21	418.2	32.4 960 7 CF591381 CF591381	CF591381 AGENCOURT
22	411.2	31.9 928 4 AL527859 AL527859	AL527859 AGENCOURT
23	409.8	31.7 688 4 BJ618816 BJ618816	BJ618816 BJ618816
24	396.2	30.7 1700 6 CR417263 CR417263	CR417263 STR0740
25	393.6	30.5 797 9 AY410030 AY410030	AY410030 Mus muscu
26	392.6	30.4 797 9 AY410028 AY410028	AY410028 Mus muscu
27	377.4	29.2 482 1 AL800329 AL800329	AL800329 AL800329
28	372.8	28.9 750 6 CF284909 CF284909	CF284909 AGENCOURT
29	365.2	28.3 797 6 CF284587 CF284587	CF284587 AGENCOURT
30	357.8	27.7 649 4 BJ033833 BJ033833	BJ033833 AGENCOURT
31	357.8	27.7 651 4 BJ625268 BJ625268	BJ625268 BJ625268
32	354.4	27.5 1065 7 U69182 U69182	U69182 U69182 Soar
33	353.6	27.4 759 7 CN083539 CN083539	CN083539 EC2B822D
34	353.6	27.4 805 4 BI763191 BI763191	BI763191 60306007
35	349.4	27.1 850 7 CN325999 CN325999	CN325999 AGENCOURT
36	349	27.0 910 6 CF220920 CF220920	CF220920 AGENCOURT
37	348.6	27.0 651 2 AW318973 AW318973	AW318973 un10630.Y
38	348	27.0 991 9 AL526385 AL526385	AL526385 AY410029 Pan trogl
39	346.6	26.8 797 9 AY410029 AY410029	AY410029 Pan trogl

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	42	342	26.5	1043	5	BX459201	BX459201
	43	337.2	26.1	787	1	AU141161	AU141161
	44	334.6	25.9	678	2	AW160750	AW160750 au75f01.Y
	45	332.6	25.8	680	4	BI761532	BI761532 603046682